



#8

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lindler, Luther E
Warren, Richard
VanDeBerg, Lillian
Rubin, Fran
- (ii) TITLE OF INVENTION: Protein From Brucella Species
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hendricks and Associates
 - (B) STREET: P.O. Box 2509
 - (C) CITY: Fairfax
 - (D) STATE: Virginia
 - (E) COUNTRY: United States
 - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/785,689
 - (B) FILING DATE: 20-FEB-2001
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hendricks, Glenna
 - (B) REGISTRATION NUMBER: 32,535
 - (C) REFERENCE/DOCKET NUMBER: lindler
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 425-8405
 - (B) TELEFAX: (703) 425-8406

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1025 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brucella

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCTGACAT AACCCGCTTT GTCCAAATTT TTTCAACTTT TCCTGTAGGA GATTTTATGA	60
ACACTCGTGC TAGCAATTTT CTCGCAGCCT CATTTTCCAC AATCATGCTC GTCGGCGCTT	120
TCAGCCTGCC CGCTTTCGCA CAGGAGAATC AGATGACGAC GCAGCCCGCG CGCATCGCCG	180
TCACCGGGGA AGGCATGATG ACGGCCTCGC CCGATATGGC CATTCTCAAT CTCTCGGTGC	240
TACGCCAGGC AAAGACCGCG CGCGAAGCCA TGACCGCGAA TAATGAAGCC ATGACAAAAG	300
TGCTCGATGC CATGAAGAAG GCCGGCATCG AAGATCGCGA TCTCCAGACA GCGGGCATCA	360
ATATCCAGCC GATTTATGTC TATCCTGACG ACAAGAACAA CCTGAAAGAG CCTACCATCA	420
CCGGCTATTC TGTATCCACC AGTCTCACGG TTCGCGTGCG CGAACTGGCC AATGTTGGAA	480
AAATTTTGA TGAATCCGTC ACGCTCGGTG TTAATCAGGG CGGTGATTTG AACCTGGTCA	540
ATGATAATCC CTCCGCCGTG ATCAACGAGG CGCGCAAGCG CGCAGTGGCC AATGCCATTG	600
CCAAGGCGAA GACGCTTGCC GACGCTGCAG GCGTGGGGCT TGGCCGTGTG GTGGAAATCA	660
GTGAACTGAG CCGCCCGCCC ATGCCGATGC CAATTGCGCG CGGACAGTTC AGAACCATGC	720
TAGCAGCCGC ACCGGACAAT TCCGTGCCGA TTGCCGCAGG CGAAAACAGC TATAACGTAT	780
CGGTCAATGT CGTTTTTGAA ATCAAGTAAA TAGCTGGGGT ATGACGCCCT TTGCCACCTG	840
ATACAAAACG CCGGCCTGGT TTCACAGGCC GGTTTTTTTG ATTAGAGCGC GTTTCGATCT	900
GATTGAATCC GATCGGCGCT CTAATCCTTT GTTTTGACGC GCATCTTTTC CGAAAACCGT	960
TTCACACTTT TCGGGATGCG GTCTAGCGGA TGATCGGGCA ACCGCGCGTA TCGGCAAATG	1020
TCACG	1025

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brucella

(B) STRAIN: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asn	Thr	Arg	Ala	Ser	Asn	Phe	Leu	Ala	Ala	Ser	Phe	Ser	Thr	Ile	
1				5					10					15		
Met	Leu	Val	Gly	Ala	Phe	Ser	Leu	Pro	Ala	Phe	Ala	Gln	Glu	Asn	Gln	
			20					25					30			
Met	Thr	Thr	Gln	Pro	Ala	Arg	Ile	Ala	Val	Thr	Gly	Glu	Gly	Met	Met	
			35				40					45				
Thr	Ala	Ser	Pro	Asp	Met	Ala	Ile	Leu	Asn	Leu	Ser	Val	Leu	Arg	Gln	
	50					55					60					
Ala	Lys	Thr	Ala	Arg	Glu	Ala	Met	Thr	Ala	Asn	Asn	Glu	Ala	Met	Thr	
65					70					75					80	
Lys	Val	Leu	Asp	Ala	Met	Lys	Lys	Ala	Gly	Ile	Glu	Asp	Arg	Asp	Leu	
				85					90					95		
Gln	Thr	Gly	Gly	Ile	Asn	Ile	Gln	Pro	Ile	Tyr	Val	Tyr	Pro	Asp	Asp	
			100					105					110			
Lys	Asn	Asn	Leu	Lys	Glu	Pro	Thr	Ile	Thr	Gly	Tyr	Ser	Val	Ser	Thr	
			115				120					125				
Ser	Leu	Thr	Val	Arg	Val	Arg	Glu	Leu	Ala	Asn	Val	Gly	Lys	Ile	Leu	
	130					135					140					
Asp	Glu	Ser	Val	Thr	Leu	Gly	Val	Asn	Gln	Gly	Gly	Asp	Leu	Asn	Leu	
145					150					155					160	
Val	Asn	Asp	Asn	Pro	Ser	Ala	Val	Ile	Asn	Glu	Ala	Arg	Lys	Arg	Ala	
				165					170					175		
Val	Ala	Asn	Ala	Ile	Ala	Lys	Ala	Lys	Thr	Leu	Ala	Asp	Ala	Ala	Gly	
			180					185					190			
Val	Gly	Leu	Gly	Arg	Val	Val	Glu	Ile	Ser	Glu	Leu	Ser	Arg	Pro	Pro	
		195					200					205				
Met	Pro	Met	Pro	Ile	Ala	Arg	Gly	Gln	Phe	Arg	Thr	Met	Leu	Ala	Ala	
	210					215					220					

Ala Pro Asp Asn Ser Val Pro Ile Ala Ala Gly Glu Asn Ser Tyr Asn
225 230 235 240

Val Ser Val Asn Val Val Phe Glu Ile Lys
245 250